WHAT IS CLAIMED IS:

- A method for analyzing the sequence of a template comprising:
 - (a) capturing\the template;
 - scanning the captured template using a primer-(b) polymerase \complex for regions of complementarity to the primer;
 - extending the primer by one or more nucleotide (C) moieties by means of a template-homology dependent extension reaction; and
- detecting the extended primer, wherein detection of the extended primer indicates the presence of one or more regions of complementarity to the primer in the captured template.

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- The method of Claim 1 wherein the primer comprises a polynuclectide of 3 to 7 bases.
- A method for analyzing the sequence of a template 20 nucleic acid according to the methods of Claim 1, wherein the steps of the method are repeated for an array of primerpolymerase complexes so that a pattern of signals is generated for the template.
- The method of Claim 3 wherein the array is an array of sequence reagents, each sequence reagent comprising:
 - a capture moiety;
 - a spacer\moiety; and (ii)
 - a primer region. (iii)

- The method of Claim 4 wherein the sequence reagents are immobilized to a solid surface.
- 6. The method of Claim 5 wherein the solid surface is glass 35 or plastic. 435/6

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7. The method of Claim 5 wherein the solid surface is a glass plate, a quartz wafer, a nylon membrane, a nitrocellulose membrane, or a silicon wafer.

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- 5 8. The method of Claim 5 wherein the solid surface is silicon class.
 - 9. The method of Claim 5 wherein the solid surface is polystyrene plastic.

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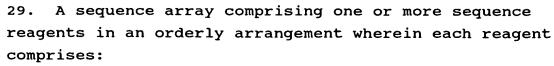
- 10. The method of Claim 4 wherein the sequence reagent further comprises an attachment moiety.
- 11. The method of Claim 10 wherein the attachment moiety is 15 located at or near the 5'-terminus of the sequence reagent.
 - 12. The method of Claim 10 wherein the attachment moiety is an amino group, a thiol group, a disulfide group, or a biotin group.

- 13. The method of Claim 4 wherein the capture moiety is on a first reagent and the primer region is on a second reagent.
 - 14. The method of Claim 13 wherein the first reagent is 25 proximal to the second reagent on a solid phase.
 - 15. The method of Claim 4 wherein the capture moiety comprises a sequence of 8-24 cytosine bases.
 - 30 16. The method of Claim 4 wherein the capture moiety comprises a specific sequence complementary to a PCR primer or a portion thereof.
- 17. The method of Claim 4 wherein the spacer region is at least 10 Å in leagth.

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- 18. The method of Claim 4 wherein the spacer region comprises a random, pseudo-random, or non-random sequence of nucleotide bases or analogs thereto.
- 5 19. The method of Claim 1 wherein the nucleotide moieties are non-chair terminating nucleotides or nucleotide analogues.
 - 20. The method of Claim 19 wherein the nucleotide moieties

 10 are deoxynucleoside triphosphate bases or ribonucleoside triphosphate bases.
 - 21. The method of Claim 1 wherein the nucleotide moiety is a chain terminating nucleotide analogue.
 - 22. The method of claim 21 wherein the chain terminating nucleotide analogue is a dideoxynucleotide.
 - 23. The method of Claim 1 wherein the nucleotide moiety is detectably labeled.
 - 24. The method of Claim 23 wherein the detectable label is a fluorescent label.
 - 25 25. The method of Claim 23 wherein the detectable label is a radioactive isotope.
 - 26. The method of Claim 23 wherein the detectable label is an electron rich molecule.
- 27. The method of Claim 1 wherein the extended primer is detected by change in mass.
 - 28. The method of Claim 4 wherein the density of sequence 35 reagents in the array is at least 1000 elements/cm².



- (i) a capture moiety which can form a stable complex with a region of a template nucleic acid molecule;
 - (ii) a spacer region; and
 - (iii) a primer region, wherein said primer region comprises 3-7 bases.

30. The sequence array of Claim 29 wherein the array comprises a set, subset, or combination of 4^3 - 4^7 different sequence reagents.

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